

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2002, 07:40:45 ; Search time 37.8 Seconds

(without alignments)  
4205.862 Million cell updates/sec

Title: US-08-153-397a-2

Perfect score: 4928  
Sequence: 1 MGPEALSLLLLLVAVSGDA.....QRPPESQLHRLADALNTV 919

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SPTREMBL\_19:\*

1: sp-archaea:\*\n2: sp-bacteria:\*\n3: sp-fungi:\*\n4: sp-human:\*\n5: sp-invertebrate:\*\n6: sp-mammal:\*\n7: sp-mhc:\*\n8: sp-organelle:\*\n9: sp-phage:\*\n10: sp-plant:\*\n11: sp-rodent:\*\n12: sp-virus:\*\n13: sp-vertebrate:\*\n14: sp-unclassified:\*\n15: sp-virus:\*\n16: sp-bacteriapi:\*\n17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4534	92.0	911	11	035407 mus musculus
2	2387	48.4	840	11	099P57 cricetus
3	1159	23.5	220	11	064108 rattus sp.
4	1044	21.2	797	5	0952V7 caenorhabd
5	1023	20.8	767	5	0952V6 caenorhabd
6	929.5	18.9	183	11	064107 rattus sp.
7	891	14.0	700	5	018433 geodia cydo
8	648	13.1	1145	5	09BK18 aplysia cal
9	633	12.8	811	13	09YH43 xenopus lae
10	631	12.8	821	13	09YH44 xenopus lae
11	628.5	12.7	486	13	09PST9 gallus gall
12	623.5	12.7	699	5	027656 geodia cydo
13	623.5	12.7	839	4	075682 homo sapien
14	615	12.5	503	4	015655 homo sapien
15	614	12.5	591	4	015656 homo sapien

17	611	12.4	767	5	018163 caenorhabd
18	608	12.3	282	13	091373 xenopus. tr
19	608	12.3	902	5	017576 caenorhabd
20	608	12.3	928	5	09BLX1 caenorhabd
21	597.5	12.1	946	13	007153 torpedo cal
22	593.5	12.0	868	11	062838 rattus norv
23	590	12.0	868	11	061006 mus musculu
24	590	12.0	871	11	061987 mus musculu
25	588.5	11.9	869	4	015146 homo sapien
26	588.5	11.9	881	11	061988 mus musculu
27	587.5	11.9	860	11	061005 mus musculu
28	584	11.9	685	5	024488 abelson mur
29	576	11.7	981	15	092809 rattus norv
30	574	11.6	168	11	092209 caenorhabd
31	571	11.6	737	5	017305 xenopus lae
32	552	11.2	354	13	09DDA2 gallus gall
33	548	11.1	989	13	09PMW6 scophthalmu
34	541.5	11.0	1245	13	03YGH8 drosophila
35	538.5	10.9	724	5	09V6K3 xenopus lae
36	529	10.7	1362	13	09PVZ4 drosophila
37	523	10.6	1504	5	09VW86 rattus norv
38	522.5	10.6	2317	11	063130 rattus norv
39	522.5	10.6	2338	11	063132 rattus norv
40	522	10.6	984	4	043718 homo sapien
41	521	10.6	1358	13	073798 xenopus lae
42	520	10.6	818	15	09PWS3 abelson mur
43	518	10.5	2340	11	064736 mus musculu
44	515	10.5	1418	13	093457 scophthalmu
45	512.5	10.4	863	5	076148 anopheles s

## ALIGNMENTS

RESULT 1  
ID 035407 PRELIMINARY; PRT; 911 AA.  
AC 035407;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE RECEPTOR-LIKE TYROSINE KINASE.  
GN NEP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=93390947; PubMed=8397369;  
RA Zerlin M., Julius M.A., Goldfarb M.;  
RT "NEP: a novel receptor-like tyrosine kinase expressed in proliferating neuroepithelia.";  
RL Oncogene 8:2731-2739(1993).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RA Zerlin M., Julius M.A., Goldfarb M.;  
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.  
DR EMBL; AF062559; AAB81866.1; .  
DR HSP; P00523; 2PTK.  
DR InterPro; IPR000719; Euk\_Pkinase.  
DR InterPro; IPR000421; FA58\_C.  
DR InterPro; IPR002011; Receptor\_tyr\_kin\_II.  
DR InterPro; IPR001245; Tyr\_Pkinase.  
DR Pfam; PF00754; F5\_P8\_type\_C; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR SMART; SM00231; FA58C; 1.

[illegible]

Dd		B81	LMEVLMCLRSGFQGLTDEQVEIENNGEPRFDGRGOYILSRPACFOITYELMLRCHSRRP	890
Oy		899	EQRPFPSQLHRLFLADALNTV	919
			:           :	
Dd		891	EQRPFPAQHRLFLDALNLT V	911
<hr/>				
RESULT	2			
O99P57	PRELIMINARY:	PRT:	840 AA.	
ID O99P57				
AC O99P57;				
DT 01-JUN-2001 (TREMBLrel_17,Created)				
DF 01-JUN-2001 (TREMBLrel_17, Last sequence update)				
DI 01-DEC-2001 (TREMBLrel_19, last annotation update)				
DE DISCOLDIN-1 DOMAIN RECEPTOR-2 (FRAGMENT).				
OS Cricetus griseus (Chinese hamster).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
CX Cricetus.				
RN NCBI_Taxid=10029;				
[1]				
RP SEQUENCE FROM N.A.				
RA Gerhardt C.C., Guillaume J.L., Strosberg A.D.;				
"Activation of the endogenous collagen receptor DDR2 by CAMP/PKA and cellular detachment in CHO/K1 cells."				
RT Submitted (DEC-2000) to the EMBL/genbank/DDJ databases.				
CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE ~ ADP + PROTEIN TYROSYNE PHOSPHATE				
-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).				
CC -1 SIMILARITY: CONTAINS 1 F5/F8 TYPE C DOMAIN.				
EMBL AF329455; AAAK01238.1; .				
HSSP P06213; 1IRK.				
DR InterPro: IPR000719; Enk_pkinase.				
DR InterPro: IPR000421; PA58_C.				
DR InterPro: IPR002011; Receptor_tyr_kin-II.				
DR InterPro: IPR001245; Tyr_PKinase.				
DR Pfam PF00069; pkinase; 1.				
DR PRINTS PR00109; TYRKINASE.				
DR SMART SMO0231; FA58c; 1.				
DR SMART SMO0220; S.TKC; 1.				
DR SMART SMO0219; Tyfrc; 1.				
PROSITE PS01285; FA58c_1; 1.				
PROSITE PS01286; FA58c_2; 1.				
PROSITE PS00011; PROTEIN_KINSE_DOM; 1.				
PROSITE PS00239; RECEPTOR_TYR_KIN-II; 1.				
KW Atg-binding; Glycoprotein; Phosphorylation; Receptor; Transferase; Transmembrane.				
NON_TER 1				
FT NON_TER 840 840				
SQ SEQUENCE 840 AA: 94950 MW: 5095656CSF53801A CRC64;				
<hr/>				
Query Match	48.4%	Score 2387;	DB 11;	Length 840;
Best Local Similarity	52.0%;	Pred. No.1,3e+181;		
Matches 478;	Conservative 115;	Mismatches 221;	Indels 106;	Gaps 16;
Oy 10 LLLLVASGDADMKGHPAKCRVALGMDRIIPSDISASSWSWDSTAHRSLRSSDG				69
	:           :           :			
Dd 6 LLLLPIIGISA--KAQNVPALICRYPLDGMGGHIIDPEITASSOWSESTARYAGRLDSBG				63
Oy 70 DGAMCPASVFEPKE-FETLYVDLRHLVLAVGTGRRAGAEGKFESKRRLRYRSRDGR				128
	:           :           :			
Dd 64 DGAACPCELPYPDDIKLEFLIDLTRLHTLVTGTRAHGAGIEAYAPMYKTINSYRDGTR				123
Oy 129 WMGKMDRAMGEYSIGNEDPEGIVLKDLGPVMVARLFREFRAPRADRVMSCLRAYELYGLMR				188
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :  :			
Dd 124 MISNRNRHGKVLDGNLSNPDYVELKDLEPPRARVRLLIPTVDHSNMANTCMRELYLGCVWL				183
Oy 189 DGLISTARPVCQTMTL--SEAVIDNDSTYYDGHVTGGLOYGGLAQULADVGLDDRFSOE				246
	:           :           :			
Dd 184 DGLVSYNPAQAQQVFLPGGSIIYLNDSVYDQ-AVGSYMTEGIQSULTDVGVGDIDEPTOTHE				242

```

OY 247 LRVMPGYDYGWNSHSSGSGYEMEFEDRLRAFOAMQVCHNNHMTLGRPGVECFR 306
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 243 YHWPGYDYGWNSHSSGSGYEMEFEDRLRAFOAMQVCHNNHMTLGRPGVECFR 301
OY 307 RGVAMMEGEPHMLNGLNDRARAVSVPLGRRVAFLOCRFLFAPWLLFSELSFIS 366
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 302 RSEASEMEPTAVSFPLVDVNSARFVYPLDDBMASAKCOYHFDATMMSEITFOS 361
OY 367 D--VYVNSPALOGTPPPAPMPPPPPTNFSLELEPPGQOVAKAEGSPAILIGLV 424
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 362 DAAMNNS-----GALPTSP-----MAPTYDMLKVDSDNTIRLLIGLV 401
OY 425 AIIILLIILALMLRMLHRRLSKAERYLEELVTHLSVPGDTILINR-----PGRE 480
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 402 AIIILLIILALMLRMLHRRLSKAERYLEELVTHLSVPGDTILINR-----PGRE 480
OY 481 P-----PPYOEPPRGNPNHSAACVPSGALLSNPAVRLLATYARPPRGCP 529
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 462 SNSTYHRIPLRPDYQP-----SRLIRLPEF----- 489
OY 530 PPRPAKPTNTQAVSGDYMEPEKPGAPLPPPPQNSVPHYAEADIVTLQGVGTGAYP 589
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 490 -----APGEESGCGSVKPAQPNP-----EGVPHYAADIYNLQGVGTGAYP 536
OY 590 ALPPGAVGDGPPRY--DFPRSLRFEKELGEGGEGVHLCEVDSPDLYSLDPLNARKH 648
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 537 ATMTLLSKRDVAEEFPFKLLTFKKMGEGGEGVHLCEVDSPDLYSLDPLNARKH 596
OY 649 PLLVAVKILRPDATKNAFSLFRNDLFEVKIMSLKDPNIIIRLGVGVQODPLCNTD 708
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 597 PLLVAVKILRADANKA-----RNDLFEVKIMSLKDPNIIIRLGVGVQODPLCNTD 708
OY 709 YWENDLNQFLSAHOLEDKAAGAPGEGGAAOGPTISYPLMLHVAQAISGMRYLATLNF 768
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 651 YWENDLNQFLSRHEPLSSCSNA-----TVSYNLKFMATQIASGMKYSLSLNF 700
OY 769 VHRDLATRNCLVGENPTIRIADFGMSRLNYAGDYRVQGRVAVLPIPMMAECLIMKFTT 828
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 701 VHRDLATRNCLVGENPTIRIADFGMSRLNYAGDYRVQGRVAVLPIPMMAECLIMKFTT 760
OY 829 ASDVAVFVTLMEVLMCLCAQPPGOLTDQVLEENAGEFFRDGGRQVYLSRPPACPOGLYE 888
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 761 AGDVAVFVTLMEVTLMEVLMCLCAQPPGOLTDQVLEENAGEFFRDGGRQVYLSRPPACPOGLYE 820
OY 889 LMLCRWSRSEQRPPFSOLH 908
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 821 LMLSCMRRETKHRPSFOETH 840
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 3
O64108 PRELIMINARY; PRT; 220 AA.
AC O64108;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE REEFOR TYROSINE KINASE (FRAGMENT).
GN PK-31.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95320273; PubMed=7597135;
RA Sakuma S., Sawa H., Iijichi A., Tofflon P.J.;
RT "Reduction induction of the receptor tyrosine kinase gene Pk-3 in
RT normal rat astrocytes";
RL Radiat. Res. 143:1-7(1995).
DR EMBL: S77585; AAB34728.1; -.
KW kinase.
FT NON_TER
SQ SEQUENCE 220 AA; 23670 MW; B9A08E5E3E43F61B CRC64;

```

```

Query Match 23.5%; Score 1159; DB 11; Length 220;
Best Local Similarity 98.6%; Pred. No. 1,7e-84;
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 404 GQOPVAKAEGSPAILIGCVAILLILLLIILALMLRMLHRRLSKAERYLEELVTHL 463
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1 GQOPVAKAEGSPAILIGCVAILLILLLIILALMLRMLHRRLSKAERYLEELVTHL 60
OY 464 SVPGDTILINRPGPREPPYOEPPRGNPNHSAACVPSGALLSNPAVRLLATYARP 523
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 61 SVPGDTILINRPGPREPPYOEPPRGNPNHSAACVPSGALLSNPAVRLLATYARP 120
OY 524 PRGPGPTPAMAKPTNTQAVSGDYMEPEKPGAPLPPPPQNSVPHYAEADIVTLQGVGTG 583
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 121 PRGPGPTPAMAKPTNTQAVSGDYMEPEKPGAPLPPPPQNSVPHYAEADIVTLQGVGTG 180
OY 584 NTYAVPALPPGAVGDGPPRYDFPRSLRFEKELGEGGEGVHLCEVDSPDLYSLDPLNARKH 623
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 181 NTYAVPALPPGAVGDGPPRYDFPRSLRFEKELGEGGEGVHLCEVDSPDLYSLDPLNARKH 220

RESULT 4
O952V7 PRELIMINARY; PRT; 797 AA.
AC O952V7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN FL1D5.3A.
GN FL1D5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None.
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Nham M.;
RT "The sequence of C. elegans cosmid FL1D5.3";
RT Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission";
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: U41532; AAK68319.1; -.
KW SEQUENCE 797 AA; 90302 MW; C96D16AFEL44899E CRC64;

Query Match 21.2%; Score 1044; DB 5; Length 797;
Best Local Similarity 29.2%; Pred. No. 1.6e-74;
Matches 273; Conservative 155; Mismatches 323; Indels 184; Gaps 31;

OY 9 LILLIILVAGSDMDMGHDPKACRALGMQDRTIPDSISASSMS-DSTARHSRLSS 67
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 3 LILLIILVAGSDMDMGHDPKACRALGMQDRTIPDSISASSMS-DSTARHSRLSS 62
OY 68 DGDGAMCPAGSVFPKEEYLVLDLQRLHLVALLVGTQGRHAGLGRFSGSYRLRYSRDC- 126
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 63 SSGSAMCPKQINSLSKEMLQISFSVDVYIIVSYEQGFDDGRGHEVATARKIQWPSL 122
OY 127 RRMGMKDRMGOEIVSGNDEGVVLLKDLGPPMAVRLVFPYPRADRVNSVCLRVELYGCL 186

```

```

Db 123 NAMASYKDFELETIPANNDEHAIRRHRLAIRIRIATVPANSYRTVCMREVEGCP 182
QY 187 WRDGLLSTAVAGCTMTLSEAVYINDSTYGHVYGLQY-GGLQGLADGVVGLDFFKQ 245
Db 183 FDDSLVFNVDQGG--LQSGISYHDSYDGNLANSPLHTGLKLDGEGKNNFVN 239
QY 246 ELRWVPGDYVGMGNHSSFGYEMEFEDRLRAFOAMOVHNNMHTLGARLPQGVCECF 305
Db 240 -----HKWVGMRK--RNGNVKLAPEFSELRNISILHTSN-----EF 276
QY 306 RRGPMAMESEPMRNLG-----NLGDP-----AAVSVPLGVARFLQCRFL 351
Db 277 KKS-AKAFSSATVLFSGNKDSDTYVHFNPNBEDTESEVPRMIRIPVNNRIAKAKIRLN 335
QY 352 FA--GFWLLESEISFIDVYV--KSSPALGCTFPAPMPPPPPTNSSLLEFRGQ 405
Db 336 FGTDSDMLFISEVNFESNHNIELLNDVYI-----PDSVSYSFVTEHDGT 382
QY 406 QPVAKAGSPALIGCTVAIIILLIILMLRLHMRRLS-----KAERVLEBELT 460
Db 383 -----SMFAPII--FFFMFLIVAVIILVLYRKREYKAKSSPNAKREIL----- 427
QY 461 VHLSPGDTLLNNRPPRPPYQEPRPGRNPHSAPCVPNGSALLLSNPAYRLLATY 520
Db 428 --LTDGNTIKHH-----VSPSTYOMAR-----DNLQNALIEKMPSPITSDY 468
QY 521 ARPRGCGPTLPAMAKPTN---QAYSGDYMEPKPGAPLPPPPONSVHYAADIYTL 577
Db 469 AEPDISVCSVTA-----NTPPLYGIDPY-DTQKRSNP-----SSMVKYSY 511
QY 578 QGVGTGNTYVAPLPAGVDDGPPRVDFPPSRRLFRKLEGEQGEVHLCEVSDPDLVS 637
Db 512 -----GEVYCT-TLP-----EIAKDCLVSRIOGEGEVDLCOLEN----- 548
QY 638 LDPEPLNRKQHPLIVAKILRPDATKNASFLPSRNDLEKVKIMSLKDPNIIRLLGVC 697
Db 549 -----RK-----VAVKKLH-----GISQADEFSFHREIRVIGSLKHPNVEVYVC 589
QY 698 VODPCLMINDYMGDGLNPLSAHQLEDKAABGAPDGOAOGPTTSYMLHVAQIA 757
Db 590 TIOKPIICIMEYENGSLKSYI-----LNKPTIQTQSCISICTOLA 630
QY 758 SGMYATLTFVHRDLATRNCLVGENFTIKIADFGMSRNLVAGDYVVOGRAVLPIMMA 817
Db 631 AGLAYLESCHFVRHDIAARNCIYDGBGNVAKIADFGMARSLXSOEYVVECKVLPIMMA 690
QY 818 WECLMGKFTTASDVNAFVGTLMEEVLMLCRAOPFGOLTDEQVIEAGEFFRDGROYLS 877
Db 691 WEALLLCKFSTASDVNMGFTVMTMEIFSLCESEKPYSDMTDDVVENLQMSSTGSLKQVLS 750
QY 878 RPACPGGLY-ELMLRQMSRESQRPFPQSOLHRL 911
Db 751 RPRCPFSKLYNEOITLPCWNTESSRFSFENVHLL 785

```

```

RESULT 5
0952V6 PRELIMINARY; PRT; 767 AA.
AC 0952V6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE HYPOPHYSEAL PROTEIN F11D5.3B.
GN F11D5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;

```

```

RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT Investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Nham M.;
RT "The sequence of C. elegans cosmid F11D5."
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41532; AK68320.1;
SQ SEQUENCE 767 AA; 86900 MW; 2953C06B9416F2EE CRC64;

Query Match 20.8%; Score 1023; DB 5; Length 767;
Best Local Similarity 29.3%; Pred. No. 7,4e-73;
Matches 266; Conservative 149; Mismatches 308; Indels 184; Gaps 31;

QY 37 MODRTIPSDISASSMS-DSTARHSRLSSDGDGAMCPAGSVFPEEETLOYDQLRL 95
Db 1 MSNRKIDEDISASSSDLOSTGPHARAOESGAMCRNQINSLSKEKLOISFSDVT 60
QY 96 LVALVGTGSHAGLGKFSRSYRLARYSRDG-RRMGKMRMGQEVISGNEDEPGVYLKD 154
Db 61 VITSVEFGFRDQGRGEMATAFRIQWRPDLNMAASYKDFELETIPANNDEHAIRRH 120
QY 155 LGPRMVARLRFYPRADRVMSVCLRVLLGCLMDGLLSTAPVQGMVYSEAYINDST 214
Db 121 LDRRIARRIRIVPVSSTRTVCMREVEFGCPDLSLVFNVDQGG--LQSGISYHDS 177
QY 215 YDGHVTVGLQY-GGLQGLADGVVGLDPPFRKSOELRWMPGVDYVGMNSHSSFGYEMEF 273
Db 178 YDGLNANSPLHTGLIGLTYGEGVKNVFNH-----HKWVGMRK--RNGNVKLAPE 228
QY 274 FDLRAFOAMOVHNNMHTLGARLPGEVECFRRGPMAMEGEMRNLG-----N 325
Db 229 FSELNRISGILIHNS-----EFKKS-AKAFSSATVLFSGNKDSDTYVH 273
QY 326 LGDPR-----AAVSVPLGVARFLQCRFLA--GFWLLESEISFIDVYV--NSS 373
Db 274 FNNPDETESEVPRMIRIPVNNRIAKVAKIRLNFDTSDMLFISEVNFESNHNIELLND 333
QY 374 PALGTPPAPMPPGPPPNFSSLELEPRGOQVAKAESPTAILIGCTVAIIILLLI 433
Db 334 VVI-----PDSVSYSFVTEHDGT-----SMFAPII--FFFMFLIVAVI 370
QY 434 IALMLRHLHMRRLS-----KAERVLEBELTVHLVSPGDTLLNNRPPRPPYQEP 488
Db 371 ILTVLYRKREYRVKASSPSPNAKREIL-----LTDGNTIKHH-----VSPSTYOMAR 418
QY 489 PRGNPPHSAPCVNGSALLLSNPAYRLLATYARPPGCPPTPAMAKPTNT---QAYSG 545
Db 419 -----DNLQNALIEKMPSPITSDYVMEPDISVCSVTA-----NTPPLYGIDG 461
QY 546 DYMEPEKPGAPLPPPPONSVPHTAADIYTLQVGTGNTYVAPLPAGVADGPPRVDF 605
Db 462 PY-DTQKRSNPL-----SSMVKYSYD-----GEVYCT-TLP-----EI 492
QY 606 PRSLRFRKELRGQGEVHLCEVSDPDLVSLDFPLNVRKQHLVAVILRPDATKNA 665
Db 493 ARDKLCVSRIOGEGEVDLCOLEN-----RK-----VAVKKLH----- 527
QY 666 SFLEFRNDLKEVKIMSLKDPNIIRLLGVCVQDDPCLMITYMNGDNLQPLSAHQLE 725
Db 528 GISQADEFSFHREIRVIGSLKHPNVEVYVGTIOKPIICIMEYENGSLKSYI----- 581
QY 726 DKAAGCAPGDGOAOGPTTSYMLHVAQIASGMYATLTFVHRDLATRNCLVGENFT 785

```

```

Db 582 -----LKNPTIOTSOCISICTQLAAGLAVLSCNPNVHDIARNLTVDEGN 628
QY 786 IRIADPGSRNLYAGDYIVVOGRANVPIRMAMAECLIKKFTTASDVNAPGVTLMVLM 845
Db 639 VRIADPGSRNLYAGDYIVVOGRANVPIRMAMAECLIKKFTTASDVNAPGVTLMVLM 845
QY 846 CKAOPFGOLTDEOVYENMEFFRDGROYVLSRPACPGGLY-ELMLRCMSRSEORPPF 904
Db 669 CSEKYSMDTDDVYENLQSMSTGSLKOVLSRPRMPSKLYNEOITLPCWNYESSRPSF 748
QY 905 SOLHREFL 911
Db 749 ENVHLHL 755

RESULT 6
ID 064107 PRELIMINARY: PRT: 183 AA.
AC 064107:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RECEPTOR TYROSINE KINASE (FRAGMENT).
GN PK-35.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95320273; PubMed=7597135;
RA Sakuma S., Saya H., Tjichi A., Tofilon P.J.;
RT "Radiation induction of the receptor tyrosine kinase gene Ptk-3 in
RT normal rat astrocytes."
RL Radiat. Res. 143:1-7(1995).
DR EMBL: S77556; AAB34729.1;
KW Kinase.
FT NOWTER 1
SQ SEQUENCE 183 AA; 19717 MW; 66DE2709B5E4A832 CRC64;

Query Match 18.9%; Score 929.5; DB 11; Length 183;
Best Local Similarity 81.8%; Pred. No. 2.6e-66;
Matches 180; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

QY 404 GQOPVAKAEGSPAILICGLVAIIILLLIITLMLRLHWRLLSKAERRVLEEELTVHL 463
Db 1 GQOPVAKAEGSPAILICGLVAIIILLLIITLMLRLHWRLLSKAERRVLEEELTVHL 60
QY 464 SVPGDTILINRPGPREPPYQEPFRGNPPHSAPCVNGSALLISNPAYRLLLTATYAR 523
Db 61 SVPGDTILINRPGPREPPYQEPFRGNPPHSAPCVNGSALLISNPAYRLLLTATYAR 103
QY 524 PRGCPPTPAMAKPTNTQAVSGDYMEKPGAPLPPPNQSVPHYAEADIVTQGVGG 583
Db 104 -----SGDIHEPKPGAPLPPPNQSVPHYAEADIVTQGVGG 143
QY 584 NTYAVPALPGAVDGPVRVDFPRSRLLRKKELGSGQFGE 623
Db 144 NTYAVPALPGAVDGPVRVDFPRSRLLRKKELGSGQFGE 183

RESULT 7
ID 018433 PRELIMINARY: PRT: 700 AA.
AC 018433:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RECEPTOR TYROSINE KINASE.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;

```

```

OC Astrophorida; Geoditidae; Geodia.
RN NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224609; PubMed=9060390;
RA Gamulin V., Skorochood A., Mueller M., Schaecke H., Mueller W.E.G.;
RT "Experimental indication in favor of the introns-late theory: The
RT receptor tyrosine kinase gene from the sponge Geodia cydonium."
RL J. Mol. Evol. 44:242-252(1997).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: X94128; CA63848.1;
DR HSSP: P08631; IAD5.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR02011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00069; pkinase_1.
DR SMART: SM00409; IG_1like; 1.
DR SMART: SM00410; IG_1like; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 700 AA; 77851 MW; 74953FC82D820B6C CRC64;

Query Match 14.0%; Score 691; DB 5; Length 700;
Best Local Similarity 32.2%; Pred. No. 2e-46;
Matches 193; Conservative 87; Mismatches 193; Indels 126; Gaps 20;

QY 409 AKAEGSPAILICGLVAIIILLLIITLMLRLHWR-----MLRLHWR----- 445
Db 136 SNSGSGNSGVINGVILITLLIITLILFVWVWYCYRRGRGFDLGSCELSGSCGCV 195
QY 446 ILSKAEKRYLEELVHLSVPGDTILINRPGPREP-----PYQEPFRGN--PPHSAP 498
Db 196 ILSKAEKRYLEELVHLSVPGDTILINRPGPREP-----PYQEPFRGN--PPHSAP 255
QY 499 CVPNGSALLISNPAYRLLLTATYARPPRGPPPTPAMAKPTNTQAVSGDYMEKPGAPLL 558
Db 256 -----LTTTELMEIEMSIDKELESPFOEKP--RRNTGLSTYSQSGTIPKLAKTKL 307
QY 559 PPPPNQSVPHYAEADIVTLQ-GVTGANT-YAVPALP----- 592
Db 308 RFFKKKRNPIYQSVLVLELELDVNTLYALPLPNSTRNSASTDLDASPIYSAIN 367
QY 593 -----FGAVD-----GP-----PRVDFPRSRLLRKKELGSGQFGEHL 627
Db 368 PSMFTKRSTSTGNDDLEHPGPIYARPIKQKMRPLSVNINIRKYQIGVQFAVVIA 427
QY 628 EYD--SPDVLSDPPLNVRKGH-----PLVAVYILRPDADTKNASFSLSNDLKEVK 680
Db 428 EYDGLSGSNVSLP-----KSNMADGVALYAVKLLPDVSDV-----RQSDKEIK 475
QY 681 ILSRLKDPNIRLLGCVQDDPLCMITIDYMENGDLNQLSAHQLDKAAEGAPGDGAQAQ 740
Db 476 FMSQLQHDHSIVQLAVCHSKHPFYMEYMENGDLNQLQKQVMD-----DSDSLY 527
QY 741 GETIYPMILHRAQDIASGMKRLATLNFVHDLARNLVGENFTIKADGMSRNTYAG 800
Db 528 SNQIPSTLLVYAQVLAGMYLSSLNHYHDLARNLVSNFRKIKSIDGMSRNLTER 587
QY 801 DYRYVQAGVAVPIRMAMAECLIKKFTTASDVNAPGVTLMVLMCKRAOPFGOLTDEQVI 860
Db 588 VYRYRGRAMPIRMALIES-FYGRFSEKSDAMAVGVTVMETIYLTKKQPIEELDDQMI 646

```

QY 861 ENAEFFRDOGROYLLSRPPACPOGLYELMLRCMSRESEORPPPSQLHRLAEDALNTV 919  
DB 647 QDA---INGTGRR-MGRPECCPOAVYEVLLFCWEYAAADRAFERKEIH-----DSLMLI 696

RESULT 8  
ID Q9BKL8 PRELIMINARY; PRT; 1145 AA.  
AC Q9BKL8;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ROR.  
OS Aplysia californica (California sea hare).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;  
OC Aplysiidae; Aplysia.  
OC NCBI\_TaxID=6500;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McKay S.E., Hislop J., Scott D., Bulloch A.G., Kaczmarek L.K.,  
RA Carew T.J., Sossin W.S.;  
RT "Aplysia tor, a member of the Trk/Musk family of receptor tyrosine  
RT kinases, forms clusters on the surface of identified neuroendocrine  
RT cells";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC EMBL: AF216782; AKK25726.1; -.  
DR HSSP: P11362; 1FGK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR000024; Fz\_domain.  
DR InterPro: IPR003598; Ig.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003600; Ig\_like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR000001; Kringle.  
DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00047; Ig\_1.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00018; KRINGLE.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00409; Ig\_1.  
DR SMART: SM00408; Ig\_c2; 1.  
DR SMART: SM00410; Ig\_like; 1.  
DR SMART: SM00130; KR; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR SMART: SM00219; Tyrc; 1.  
DR PROSITE: PS50038; Fz; 1.  
DR PROSITE: PS50021; KRINGLE\_1; UNKNOWN\_1.  
DR PROSITE: PS50070; KRINGLE\_2; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;  
KW Receptor; Transferase; Transmembrane.  
SQ SEQUENCE 1145 AA; 123622 MW; 5C49FA6E2A9D1ABD CRC64;

Query Match 13.1%; Score 648; DB 5; Length 1145;  
Best local Similarity 31.8%; Pred. No. 1,le-42;  
Matches 187; Conservative 74; Mismatches 149; Indels 176; Gaps 24;

QY 445 RLISAKERYLEEL--YVHL-----SVPGDTLLIN-----NRGPRE-----PPPY 484  
DB 310 RKICRDEALENDICRTETELAKRHNLIGDNLPCRSQLOGGTRGDCNICRIGMPGS 369  
QY 485 QERPR---GNPHSAPCPVNSALLSNPAYLLATATAPRR---GPGPPPAK-- 536  
DB 370 TSGRGKPKGNGPSWNP-----GTRDPPRGSGSGSKRPTSDKDT 410

QY 537 -----PTNQAVSG-----DYMEPE-----KPGAP 556  
DB 411 GRGGGPTDYCYCGRGNINGEVSVSKSGFMCLGMDSGFELGDHNYCANPNCREAP 470  
QY 557 LL-----PPPNQSV-----HYAADIIVLTQVGTGNT---YAVPALP-PGAVG- 597  
DB 471 WCFNDRKMPKELCAVPCSDYDEGHSEAD-----EGSNKLMYILIPSLTVPLALGI 523  
QY 598 -----DGPDRDFRSRLREFEKLGEQGF 622  
DB 524 LLALICQKSHNTRASRPNNKQAPVEMSPLNPKSASRAREFPMPNIRFLOELGEGAFG 583  
QY 623 EVHLCEYDSDPDVSLDFPLNVRKGPLLVAVKILRPDATTNKSFLSRNDFLEKVIY 682  
DB 584 KVVYGE-----LVGLGESSV-----TTVAIKLKEVALKV-----QNDPREVDLM 626  
QY 683 SRLKPNIIIRLLGVGVODDPLCMITDYEMENDLNOFLSAH--QLEKKAEGAPDGOAAQ 740  
DB 627 SDMHNPVIVCLGVCMKQEPWCMLEFYMAQGDLEHLLSPHSBDVYFAEDDSGTG--G 683  
QY 741 GPITSYMLHVAQIASGMRYLATLNFVRHDLATRNCLVGEENTTIKADGMSRLYAG 800  
DB 684 GHILEYSEMHLVSTOVAAGMEYLASHFVHRDLAARNILVADGLVXISDGLSRDYSS 743  
QY 801 DYRVQGRAVLPFRMAMECTIMGKFTTASDVMAFGVTLFVLMCRAPGOLDEQVI 860  
DB 744 DYIVQSKSLPVMMPPEALILYKFTTDSVMAFGVYLVMEVSY-GLOPTYGSSNOEVI 802  
QY 861 ENAEFFRDOGROYLLSRPPACPOGLYELMLRCMSRESEORPPPSQLH 908  
DB 803 EMI-----RSQR-LGCPCECPARIYIGLVMECHHEMPARRPPREIH 843

RESULT 9  
ID Q9YH43 PRELIMINARY; PRT; 811 AA.  
AC Q9YH43;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.  
GN XTRKB.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Piploidea; Piploidea;  
OC Xenopodinae; Xenopus.  
OC NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Islam N., Gagnon F., Moss T.;  
RT Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
RT mRNA are expressed in a pseudo-segmental manner within the early  
RT xenopus central nervous system.\*;  
RL Int. J. Dev. Biol. 40:973-983(1996).  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC EMBL: U39671; AAD00002.1; -.  
DR HSSP: P06213; 1IRK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Cterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00560; LRR; 1.  
DR Pfam: PF01463; LRRT; 1.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00409; Ig; 1.

DR SMART; SM00082; LRRT; 1.  
 DR SMART; SM00013; LRRT; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 KM Transmembrane; Tyrosine-protein kinase  
 SQ SEQUENCE 811 AA; 91249 MW; C67CDICF132C1CF5 CRC64;

Query Match 12.8%; Score 633; DB 13; Length 811;  
 Best Local Similarity 44.7%; Pred. No. 1e-41;  
 Matches 139; Conservative 48; Mismatches 80; Indels 44; Gaps 9;

QY 607 RSRLEFEKELGEGQFGEVHLCE---VDSPODLSLDFPLNVRKGHPPLVAVKILRPDATK 663  
 DB 524 RHNIIVLKRLEIGEGAFGKFLAECYNLYPEDD-----KILVAVKTLK-DASD 568  
 QY 664 NASFSLSRNDPLKEVKIMSLKDPNIRILGVCVQDDPLCMITDYMENGDLNQLSAHQ 723  
 DB 569 NA-----RDFRREKELLTNLQHEHIVKFGVCVEGDPIMVEYMKHGDINKFLRAH- 621  
 QY 724 LEDKAAEGAPGDGQAAG---PTISYPMILHVAQAISGMYLATLNFVHDLATRNCLV 780  
 DB 622 -----GPDVAVLAEGRNPAELTQSOMLHIAQIAAGMYILASQFVHHDLATRNCLV 673  
 QY 781 GENFTIKIADFGMSRLNAGDYRYVOGRAVLPIRMAMECTILMGKFTTASDVAFGYTLW 840  
 DB 674 GEMLVKIRIGFGMSRDYSDYRYVGHTMLPIRMMPESIMYKFTTESVMSLGYVLW 733  
 QY 841 EVLMICRAQPFQGLTDOVIEENAGEFFRDGROYLISRPACPGKLYELMRCRSRESEQ 900  
 DB 734 EIFTYGR-QPMYQLSNNEVEICT-----TQGR-VLQRPRTCPREYVDLMGCMQRPBHM 785  
 QY 901 RPPFSQLRFL 911  
 DB 786 RLNIKEIHSIL 796

RESULT 10  
 Q9YH44 PRELIMINARY; PRT; 821 AA.  
 AC Q9YH44: 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.  
 GN XTRKB.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97101727; PubMed-8946245;  
 RA Islam N., Gagnon F., Moss T.;  
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
 RT mRNA are expressed in a pseudo-segmental manner within the early  
 RT Xenopus central nervous system.";  
 RL Int. J. Dev. Biol. 40:973-983(1996).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL; U39670; AA000001.1; -;  
 DR HSSP; P06213; IIRK.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR003599; 19.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.

DR InterPro; IPR002011; Receptor\_tyr\_kin\_II.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00560; LRR; 1.  
 DR Pfam; PF01463; LRRT; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00082; LRRT; 1.  
 DR SMART; SM00013; LRRT; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 KM Transmembrane; Tyrosine-protein kinase.  
 SQ SEQUENCE 821 AA; 92311 MW; 0AF81BE74F08FED3 CRC64;

Query Match 12.8%; Score 633; DB 13; Length 821;  
 Best Local Similarity 44.7%; Pred. No. 1e-41;  
 Matches 139; Conservative 48; Mismatches 80; Indels 44; Gaps 9;

QY 607 RSRLEFEKELGEGQFGEVHLCE---VDSPODLSLDFPLNVRKGHPPLVAVKILRPDATK 663  
 DB 534 RHNIIVLKRLEIGEGAFGKFLAECYNLYPEDD-----KILVAVKTLK-DASD 578  
 QY 664 NASFSLSRNDPLKEVKIMSLKDPNIRILGVCVQDDPLCMITDYMENGDLNQLSAHQ 723  
 DB 579 NA-----RDFRREKELLTNLQHEHIVKFGVCVEGDPIMVEYMKHGDINKFLRAH- 631  
 QY 724 LEDKAAEGAPGDGQAAG---PTISYPMILHVAQAISGMYLATLNFVHDLATRNCLV 780  
 DB 632 -----GPDVAVLAEGRNPAELTQSOMLHIAQIAAGMYILASQFVHHDLATRNCLV 683  
 QY 781 GENFTIKIADFGMSRLNAGDYRYVOGRAVLPIRMAMECTILMGKFTTASDVAFGYTLW 840  
 DB 684 GEMLVKIRIGFGMSRDYSDYRYVGHTMLPIRMMPESIMYKFTTESVMSLGYVLW 743  
 QY 841 EVLMICRAQPFQGLTDOVIEENAGEFFRDGROYLISRPACPGKLYELMRCRSRESEQ 900  
 DB 744 EIFTYGR-QPMYQLSNNEVEICT-----TQGR-VLQRPRTCPREYVDLMGCMQRPBHM 795  
 QY 901 RPPFSQLRFL 911  
 DB 796 RLNIKEIHSIL 806

RESULT 11  
 Q9PST9 PRELIMINARY; PRT; 486 AA.  
 AC Q9PST9: 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE NEUROTROPHIN RECEPTOR B XTRKB-BETA (FRAGMENT).  
 GN XTRKB.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97101727; PubMed-8946245;  
 RA Islam N., Gagnon F., Moss T.;  
 RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
 RT mRNA are expressed in a pseudo-segmental manner within the early  
 RT Xenopus central nervous system.";  
 RL Int. J. Dev. Biol. 40:973-983(1996).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

DR EMBL: U39672; AAD09444.1; --  
 DR HSP: P06213; LRR.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
 DR InterPro: IPR001245; tyr\_pkinase.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00219; TyrcK.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR.1.  
 DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II.1.  
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 KW Transmembrane; Tyrosine-protein kinase.  
 FT NON-TER  
 SQ SEQUENCE 486 AA; 54546 MW; 1645B69ABE78274F0 CRC64;

Query Match 12.8%; Score 631; DB 13; Length 486;  
 Best Local Similarity 44.1%; Pred. No. 7.1e-42;  
 Matches 137; Conservative 50; Mismatches 80; Indels 44; Gaps 9;

QY 607 RSRLNFKELGEGFGEVHLCEVDS---PDLVSLDFPLNVRKQHPILVAVKILRPDATK 663  
 Db 199 RHNIVLKELEGAGFAGKVFLECYNLYLEQD-----KIIVAYKTLK-DASD 243  
 QY 664 NASLSLFRNDFLEKVKMSRKADPNIRLLGVCVQDDPLCMITDYMENGDLNPLSAHQ 723  
 Db 244 NA-----RKDFHREAEILLTNLOHENTYKFGYCVCEGDPILNVEFVKGDLNFKLRAH- 296  
 QY 724 LEDKAAEGAPGDGAAGS---PTISYPLMLVAAQIASGMVLYATLNVVHDLTRNCLV 780  
 Db 297 -----GPAVLAEBENLAEITQSOMHIISQILAGMYLLASQHHVHDLTRNCLV 348  
 QY 781 GENFTIKIADFGSRNLLVAGDYRVQGRAVLPIRMAMECTLMKFTTASDVMAFGVYLM 840  
 Db 349 GENLIVKIGDGMGRDYSTDYRVGHTMLPIRMMPESIMYRFTTESVMSGLVYLM 408  
 QY 841 EVMILCRAGPFGQLTDEVIYNAEFPDQGRVYLSRPPACPGGLYELMIRCSRESEQ 900  
 Db 409 EITFYGK-QPMYQLSNNEVICI-----TQGR-VLQRPRTCPKEIYDLMIGMCQREPHM 460  
 QY 901 RPPFSQLHRL 911  
 Db 461 RLNIKEIHSLL 471

RESULT 12  
 Q090699 PRELIMINARY; PRT; 790 AA.  
 ID 090699  
 AC 090699  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)  
 DE 01-DEC-2001 (TEMBLrel. 19, last annotation update)  
 DE TPPOWYOSIN RECEPTOR KINASE.  
 GN CYRKA.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 OX [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Schreyer A., v Schack D., Dechant G., Barde Y.A.;  
 RT "Early expression of the nerve growth factor c-tyrA in chicken  
 RT sympathetic and sensory ganglia.";  
 RL Mol. Cell. Neurosci. 6:0-0(0).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL: U43396; AAA85289.1; --  
 DR HSP: P11362; IFGR.  
 DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
 DR InterPro: IPR001245; tyr\_pkinase.  
 DR Pfam: PF00047; Ig.1.  
 DR Pfam: PF00560; LRR.2.  
 DR Pfam: PF01463; LRRCT.1.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00409; IG.1.  
 DR SMART: SM0082; LRRCT.1.  
 DR SMART: SM00219; TyrcK.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM.1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR.1.  
 DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II.1.  
 DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;  
 KW Transferase; Transmembrane; Tyrosine-protein kinase.  
 SQ SEQUENCE 790 AA; 88669 MW; AD2314608F30AD71 CRC64;

Query Match 12.8%; Score 628.5; DB 13; Length 790;  
 Best Local Similarity 30.6%; Pred. No. 2.3e-41;  
 Matches 193; Conservative 78; Mismatches 188; Indels 171; Gaps 23;

QY 356 MLFSEISFIDVYNNSSPALGTFPPAPMPPGPPPNFSSLELEPPGQGVAKAESSP 415  
 Db 237 WEVLEINNISSSLNHK-----DLTCAENAVGLAEDS- 269  
 QY 416 TAILIGCVAILLLILLIALLMLRHLNR-----RLSKAERVLEETVHLV--- 465  
 Db 270 -VMLNVTFPPVILLSEAILPQHFNCIPESVDNPTRLMLFNSGMLPEGYIHRIYEV 328  
 QY 466 -PGTILIN---NRGPREPPYQEPKPNPPHSACVNGS-ALLSNP---AYRL 516  
 Db 329 EPNSTVHLGCLQLRN-----PH---VNNGVYTLVQNPDLGRATRSI 367  
 QY 517 LATYARPP--RGPPPTPAWAKPTNTQAYSGDYMEPEKGAFLPPPPNSVPHYAEDI 574  
 Db 368 QGRFMDNPFSSPEEPILPVISPLGTRNS-----LEGPEYEDHETFGVSV 414  
 QY 575 VTQGV-----TGNTYAVPA-----LPPGAVGDP 600  
 Db 415 AVALAFAFLSVMLIALNKGRSKFGINRSVAVLAQEDDLAMSLHFMNGSSPVSTE 474  
 QY 601 PRVD-----PPSRRLRFKKELGEGFGEVHLCEVDS--PDLVSL 638  
 Db 475 SKLDGLKSNFLENPOYFCNMCVHHQRRDYLKWELEGAGFVLECSHLPEQ---- 530  
 QY 639 DFLNVRKQHPILVAVKILRPDATKNASFLSNDLKEKIKMSRLKDPNIITLLGCV 698  
 Db 531 -----EKLVAVALK-EVTESA-----RLDQREAEILLTNLOHENTYKFGYCV 574  
 QY 699 QDDPLCMITDYMENGDLNPLSAHQLEDKAAEGAPGDGAAGPTISYPLMLHVAQIAS 758  
 Db 575 EGEPLIVFEYMKRGDLNRLFLRSHGPDAKIID--QGQGGPGQGLTLH--MLQATQIAS 630  
 QY 759 GMRYLATLVVHDLATRNCLVGENFTIKIADFGSRNLLVAGDYRVQGRAVLPIRMMP 818  
 Db 631 GMVYLAHLVHDLATRNCLVGHDLVYKIGDFMSHDISTDYRVGGRMLPIRMMP 690  
 QY 819 ECLMGKFTASDVMAFGVTLMEVLMCRAPFGQLTDEVIYNAEFPDQGRVYLSR 878  
 Db 691 ESILYKRFETTESDMSGVVLMELFTYKQ-QPMYQLSNTEAIECI-----TQGR-LE 742  
 QY 879 PPAPOGLYELMIRCSRESEGRPPFSOLH 908  
 Db 743 PTPCPSEVYDIMSQWREPOQRORIDIH 772

RESULT 13



027656 ID 027656 PRELIMINARY: PRT: 699 AA.

AC 027656:

DT 01-NOV-1996 (TREMBLER. 01, Created)

DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)

DE SPOUGE RECEPTOR TYROSINE KINASE (EC 2.7.1.112).

GN GCR 2.

OS Geodia cydonium (Sponge)

OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;

OC Astrophorida; Geodidae; Geodia.

/OX NCBI\_TaxID=6047;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95142935; PubMed=7840899;

RA Gamulin V., Rinkewich B., Schaecke H., Kruse M., Mueller I.M., Werner E.G.;

RT "Cell adhesion receptors and nuclear receptors are highly conserved from the lowest metazoa (marine sponges) to vertebrates."

RL Biol. Chem. Hoppe-Seyler 375:583-588(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95251882; PubMed=7734153;

RA Schaecke H., Rinkewich B., Gamulin V., Mueller I.M., Mueller W.E.G.;

RT "Immunoglobulin-like domain is present in the extracellular part of the receptor tyrosine kinase from the marine sponge Geodia cydonium."

RL J. Mol. Recognt. 7:273-276(1994).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97224609; PubMed=9060390;

RA Gamulin V., Skorkhod A., Mueller M., Schaecke H., Mueller W.E.G.;

RT "Experimental indication in favor of the introns-late theory: the receptor tyrosine kinase gene from the sponge Geodia cydonium."

RL J. Mol. Evol. 44:242-252(1997).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

DR EMBL: X77528; CA54663.1; -.

DR HSP: P08631; IAD5.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR003599; 1g.

DR InterPro: IPR003600; 1g\_1like.

DR InterPro: IPR003006; 1g\_MHC.

DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.

DR InterPro: IPR001245; Tyr\_pkinase.

DR Pfam: PF00047; 1g; 1.

DR Pfam: PF00069; pkinase; 1.

DR SMART: SM00409; IG\_1like; 1.

DR SMART: SM00410; IG\_1like; 1.

DR SMART: SM00219; TYKC; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.

KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Transmembrane; Tyrosine-protein kinase.

SO SEQUENCE 699 AA; 77477 MW; 80A8B25AB0851CCE CRC64.

Query Match 12.7%; Score 623.5; DB 5; Length 699;

Best Local Similarity 31.6%; Pred. No. 4.8e-41;

Matches 195; Conservative 83; Mismatches 176; Indels 163; Gaps 26;

QY 409 AKAGSPALLIGCLVALILLILLIAL-MLMRLHRRLLSKARRVLEELTVHLS-- 464

DB 136 SNSSGSGNAGVILITLILILILIFVWVVCYR-----RGKLDLSCRELSCG 189

QY 465 ----VPGDTILINRGRREPPYQEPGRGPHSACVPGSALLLS----- 509

DB 190 SCSCVP-----LLALKGVKLPTRRHENDK-----NGTLRLNERNHADIYNT 234

QY 510 --NPAYRLLATYARPPGPGP-----TPAMAKPT--NT--QAY 543

DB 235 IYVAVKPLKIKISPP--PLDPLLTETELNELTSDKEKELSLIOEKPTRRNTGLSTY 292

QY 544 SCDIMEPEKPGAPLLPPPPONSVPHYAEADIVTLQ-GVTGGNT-YAVPALP----- 592

DB 293 SOSGTTIPKLRKLRKFRKKENPIYQSADELELELDVNDLTLYALPSKPNSTRNSASP 352

QY 593 -----FGAVD-----GP-----PRVDEPRRLRP 612

DB 353 TDLIASDPIYSVAIINSMFTKRSSTIGNDLDPHYGYIYARPIKOKRPOPLNYSVDNIRE 412

QY 613 KERKIGEGFGEVHLCEVD--SPDIVSLDPEPLVRKSH-----PLVAVKILRPDARKNA 665

DB 413 VKQIGVGFAPAVVLAETGTSGSNVSLP-----KSNMADGVALYAAKLPDYSDXY 466

QY 666 SFSLFSRNDFLKVKYKIMSRUKDNIIRLLGVCYQDDPLCMITDYMENGDLNQLSAHQLE 725

DB 467 LQS-----FDKRIKFSQSLQHDHSIVQLLACIHSKHPFIYMEYMEGDLNGLQYQYMW 520

QY 726 DKRAEFGAPGGOAAGPTIYPIHLHYAAQIASGMRYLATLNFVHDLATRNCLVGENPT 785

DB 521 D-----DSSALYSNQIPPSLTYMAVOIASGMVYLSLNTVHRLATRNCLVGSNFR 572

QY 786 IKIADFGMSRLYAGDYRYVQGRAVLPIRMAMECTILMGKFTTASDVAFGVTLMREYLM 845

DB 573 IKISDGMKRLNLYERYRYRGRAPLPIRMAYES-FYGFSSKSDAMAGVYWEIYTL 631

QY 846 CRAQPFQGLTDEQVIENAGFEFFDQGRVYLSNP---PACQGLYELMLRCWSRESEORP 902

DB 632 GKQPFYEELDDQDMQDA---IRGTGRRI-MGRPRVAGCVRG---AIRCWYAAADRA 683

QY 903 PFSQRLRFLEADLNTV 919

DB 684 TFEIRH----DSLNDI 695

RESULT 14

075682 ID 075682 PRELIMINARY: PRT: 839 AA.

AC 075682:

DT 01-NOV-1998 (TREMBLER. 08, Created)

DT 01-NOV-1998 (TREMBLER. 08, Last sequence update)

DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)

DE TRKC PROTEIN.

GN TRKC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98449483; PubMed=9778053;

RA Ichno N., Rodriguez R., Martin-Zanca D., Gonzalez-Sarmiento R.;

RT "Genomic characterization of the human trkc gene."

RL Oncogene 17:1871-1875(1998).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

DR EMBL: AJ224521; CA112029.1; -.

DR EMBL: AJ224522; CA112029.1; JOINED.

DR EMBL: AJ224523; CA112029.1; JOINED.

DR EMBL: AJ224524; CA112029.1; JOINED.

DR EMBL: AJ224525; CA112029.1; JOINED.

DR EMBL: AJ224526; CA112029.1; JOINED.

DR EMBL: AJ224527; CA112029.1; JOINED.

DR EMBL: AJ224528; CA112029.1; JOINED.

DR EMBL: AJ224529; CA112029.1; JOINED.

DR EMBL: AJ224530; CA112029.1; JOINED.

DR EMBL: AJ224531; CA112029.1; JOINED.

DR EMBL: AJ224532; CA112029.1; JOINED.

DR EMBL: AJ224533; CA112029.1; JOINED.

DR EMBL: AJ224534; CA112029.1; JOINED.

DR EMBL: AJ224535; CA112029.1; JOINED.

DR HSP: P06213; TRK.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro; IPR003589; Ig.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cleav.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR002011; Receptor\_Tyr\_Kin\_II.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00047; Ig\_1.  
 DR Pfam; PF00560; LRRCT; 2.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR SMART; SM00409; Ig; 1.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 KW Transmembrane; Tyrosine-protein kinase.  
 SQ SEQUENCE: 839 AA; 94428 MW; 7FE846830083C08 CRC64;

Query Match 12.7%; Score 623.5; DB 4; Length 839;  
 Best Local Similarity 31.7%; Pred. No. 6.3e-41;  
 Matches 174; Conservative 67; Mismatches 131; Indels 177; Gaps 20;

OY 490 RGNPSPASACVPRG-----SALLSNPA-----YRLLATYR 522  
 DB 326 RGNPPTLMLHNGOPRLRSKIIHVEYOGELISEGLFNKPTHYNNQNTLI-----K 381  
 OY 523 PRGPSPPTPAMAKPNTQAYSQDME---PEKGPALF---PPRPNQSVPTAADIY 575  
 DB 382 NPLG-----TANQTINGHFLKEPPESTDNFLLFDEVSPPTPTVTHKPEEDIF 430  
 OY 576 TLQVGTGNTAVPAL-----P 592  
 DB 431 GVSINAGLAACVLLVLFVMIKYGSRKFGMKPFAVISGEEDSASPLHHINHT 490  
 OY 593 PGAVGDP-----PRVDFP-----NSRLFKKELGEGQRT 622  
 DB 491 PSSLDAGPPTVYIGMTRIVYENPOYRQGHNCHEKPDYVONIKRDIYALKRELGGAGF 550  
 OY 623 EYHLCVSDPDLVSLDFPLNVRKGHPLVAVKILRPDAFKNASFSLSRNDFLKEVKIM 682  
 DB 551 KYPLAAC-----YLSPTK-DKMLVAVKALK-DPT-----LAARKDQREAEILL 592  
 OY 683 SRLKDPNIRLLGVQVODPLCMITDYMENGLNQLSAHOLEDKAAEGAPG-----DQ 737  
 DB 593 TNLQHEHYKFGVCGDGPLNMFVEYMKHGDNLKFLRAH-----GPDAMILVDSQ 643  
 OY 738 AAGGP-TISYPMILHVAAGIASGRIATLNFVHDLATRNCLVGNFTIKIADFGMSRN 796  
 DB 644 PROAKGELISOMLHIASQIASGMVYLASHQHFVHDLATRNCLVGNFTIKIADFGMSRD 703  
 OY 797 LVAGDYR-----VQGRAVLPIRMMAECILMGKFTTASDVMAFGVTLMEV 842  
 DB 704 VSTDYTRLFNPSGNDPCWCEYGGHTMLPIRMMPRESIMKRTTSDVMSFGVTLMEI 763  
 OY 843 LMLCRAQPGQLTDEQVLENAGEFFRDGROYLLSRPACPOGLYELMLRCMSRESEORP 902  
 DB 764 FTYGR-QPWFQLSNTEVICI-----TQGR--VLEPRVCPREVVDVLMGCMQREPOQL 815  
 OY 903 PFSQHLRL 911  
 DB 816 NIKELIKIL 824

RESULT 15  
 ID 015655 PRELIMINARY; PRT; 503 AA.

AC Q15655;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 55 KDA PROTEIN.  
 GN TRK-T1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92195650; PubMed-1532241;  
 RA Greco A., Pierotti M.A., Bongarzone I., Pagliardini S., Lanzl C.,  
 RA Della Porta G.;  
 RT "TRK-T1 is a novel oncogene formed by the fusion of TPR and TRK genes  
 RT in human papillary thyroid Carcinomas.";  
 RL Oncogene 7:237-242(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92175499; PubMed-1541391;  
 RA Hill K., Boone C., Goebel M., Puccia R., Sdicu A.M., Bussey H.;  
 RT "Yeast KRE2 Defines a new gene family encoding probable secretory  
 RT proteins, and is Required for correct N-Glycosylation of proteins.";  
 RL Genetics 130:273-283(1992).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL; X62947; CAA4719.1; -.  
 DR HSSP; P11362; IFGR.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002011; Receptor\_Tyr\_Kin\_II.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;  
 KW Transmembrane; Tyrosine-protein kinase.  
 SQ SEQUENCE 503 AA; 58174 MW; 17273FF47557E2FD CRC64;

Query Match 12.5%; Score 615; DB 4; Length 503;  
 Best Local Similarity 45.2%; Pred. No. 1.4e-40;  
 Matches 138; Conservative 45; Mismatches 86; Indels 36; Gaps 9;

OY 607 RSLRFRKELGEGQFGEVHLCEYDS---PODLVSLDFPLNVRKGHPLVAVKILRPDATK 663  
 DB 214 RDIYAKMLGELGAEAFKQVLAECNLLPRED-----KMLVAVK-----ALK 254  
 OY 664 NASESLFSRNDPLKEVKINSRLKDPNIRLLGVQVODPLCMITDYMENGLNQLSAHO 723  
 DB 255 EASES--ARQDQREAEELTMLQHOHIVFFGCTGRLMVFEEYMRHGDLLRFLRSIG 312  
 OY 724 LEDKAEGAPGQGAAGGTISYPMILHVAAGIASGRIATLNFVHDLATRNCLVGN 783  
 DB 313 PDKKLAGEE--DVAPGP-LGIGQLLAVASOVAAGMVTLAGLHFVHDLATRNCLVGQ 368  
 OY 784 FTIKIDFGMSRNLVAGDYRVQGRAVLPIRMMAECILMGKFTTASDVMAFGVTLMEV 843  
 DB 369 LVYKIDFGMSRNDIYTDVYRGGRTMLPIRMMPRESIMKRTTSDVMSFGVTLMEI 428  
 OY 844 MLCRAQPGQLTDEQVLENAGEFFRDGROYLLSRPACPOGLYELMLRCMSRESEORP 903  
 DB 429 TYGR-QPWFQLSNTEAIDCI-----TQGR--LEPRACPEVYALRMGCMQREPOQRS 480  
 OY 904 FSQLH 908  
 DB 481 IKDVH 485

Mon Oct 7 15:50:49 2002

us-08-153-397a-2.rspt

Page 11

Search completed: October 4, 2002, 07:45:30  
Job time: 285 sec